



JFW PCT

RAW SEQUENCE LISTING

DATE: 01/15/2004

PATENT APPLICATION: US/09/914,053A

TIME: 13:57:46

Input Set : A:\-20-3.app

Output Set: N:\CRF4\01152004\I914053A.raw

3 <110> APPLICANT: Jegla, Timothy James
 4 Wickenden, Alan
 5 Liu, Yi
 6 ICAgen, Inc.
 8 <120> TITLE OF INVENTION: BK Beta Subunits of Slo Family Potassium Channels
 10 <130> FILE REFERENCE: 018512-002030US
 12 <140> CURRENT APPLICATION NUMBER: US 09/914,053A
 > 13 <141> **CURRENT FILING DATE: 2002-04-03**
 15 <150> PRIOR APPLICATION NUMBER: US 60/121,224
 16 <151> PRIOR FILING DATE: 1999-02-23
 18 <150> PRIOR APPLICATION NUMBER: US 60/163,367
 19 <151> PRIOR FILING DATE: 1999-11-03
 21 <150> PRIOR APPLICATION NUMBER: WO PCT/US00/04441
 22 <151> PRIOR FILING DATE: 2000-02-22
 24 <160> NUMBER OF SEQ ID NOS: 19
 26 <170> SOFTWARE: PatentIn Ver. 2.1
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 29 <211> LENGTH: 257
 30 <212> TYPE: PRT
 31 <213> ORGANISM: Homo sapiens
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 34 <223> OTHER INFORMATION: BK beta 2
 36 <400> SEQUENCE: 1
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 38 1 5 10 15
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 41 20 25 30
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 44 35 40 45
 46 Leu Met Phe Phe Leu Leu Gly Thr Thr Ile Leu Lys Pro Phe Met Leu
 47 50 55 60
 49 Ser Ile Gln Arg Glu Glu Ser Thr Cys Thr Ala Ile His Thr Asp Ile
 50 65 70 75 80
 52 Met Asp Asp Trp Leu Asp Cys Ala Phe Thr Cys Gly Val His Cys His
 53 85 90 95
 55 Gly Gln Gly Lys Tyr Pro Cys Leu Gln Val Phe Val Asn Leu Ser His
 56 100 105 110
 58 Pro Gly Gln Lys Ala Leu Leu His Tyr Asn Glu Glu Ala Val Gln Ile
 59 115 120 125
 61 Asn Pro Lys Cys Phe Tyr Thr Pro Lys Cys His Gln Asp Arg Asn Asp
 62 130 135 140
 64 Leu Leu Asn Ser Ala Leu Asp Ile Lys Glu Phe Phe Asp His Lys Asn
 65 145 150 155 160

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67 Gly Thr Pro Phe Ser Cys Phe Tyr Ser Pro Ala Ser Gln Ser Glu Asp
68          165          170          175
70 Val Ile Leu Ile Lys Lys Tyr Asp Gln Met Ala Ile Phe His Cys Leu
71          180          185          190
73 Phe Trp Pro Ser Leu Thr Leu Leu Gly Gly Ala Leu Ile Val Gly Met
74          195          200          205
76 Val Arg Leu Thr Gln His Leu Ser Leu Leu Cys Glu Lys Tyr Ser Thr
77          210          215          220
79 Val Val Arg Asp Glu Val Gly Gly Lys Val Pro Tyr Ile Glu Gln His
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98 ctatgatgtgc acaagaggct gccatccagt actggagagg accgagccgt gatgctgggg 120
99 tttgccatga tgggcttctc agtctaatag ttcttcttgc tcggaacaac cattctaaag 180
100 ccttttatgc tcagcattca gagagaagaa tcgacctgca ctgccatcca cacagatatc 240
101 atggacgact ggctggactg tgccttcacc tgtggtgtgc actgccacgg tcaggggaag 300
102 taccgtgtgc ttcagggtgt tgtgaacctc agccatccag gtcagaaagc tctcctacat 360
103 tataatgaag aggtgttcca gataaatccc aagtgtcttt acacacctaa gtgccaccaa 420
104 gatagaaatg atttgcctca cagtgtctctg gacataaaaag aattcttcga tcacaaaaat 480
105 ggaacccccct tttcatgctt ctacagtcca gccagccaat ctgaagatgt cattcttata 540
106 aaaaagtatg accaaatggc tatcttcacc tgtttatattt ggcttccact gactctgcta 600
107 ggtggtgccc tgattgttgg catggtgaga ttaacacaac acctgtcctt actgtgtgaa 660
108 aaatatagca ctgtagtcag agatgaggta ggtggaaaag taccttatat agaacagcat 720
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124 Ser Ile Arg Leu Gly Leu Phe Leu Ile Ile Ser Gly Val Val Ser Leu
125          20          25          30
127 Phe Ile Phe Gly Phe Cys Trp Leu Ser Pro Ala Leu Gln Asp Leu Gln
128          35          40          45
130 Ala Thr Glu Ala Asn Cys Thr Val Leu Ser Val Gln Gln Ile Gly Glu
131          50          55          60
133 Val Phe Glu Cys Thr Phe Thr Cys Gly Ala Asp Cys Arg Gly Thr Ser

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134 65          70          75          80
136 Gln Tyr Pro Cys Val Gln Val Tyr Val Asn Asn Ser Glu Ser Asn Ser
137          85          90          95
139 Arg Ala Leu Leu His Ser Asp Glu His Gln Leu Leu Thr Asn Pro Lys
140          100          105          110
142 Cys Ser Tyr Ile Pro Pro Cys Lys Arg Glu Asn Gln Lys Asn Leu Glu
143          115          120          125
145 Ser Val Met Asn Trp Gln Gln Tyr Trp Lys Asp Glu Ile Gly Ser Gln
146          130          135          140
148 Pro Phe Thr Cys Tyr Phe Asn Gln His Gln Arg Pro Asp Asp Val Leu
149 145          150          155          160
151 Leu His Arg Thr His Asp Glu Ile Val Leu Leu His Cys Phe Leu Trp
152          165          170          175
154 Pro Leu Val Thr Phe Val Val Gly Val Leu Ile Val Val Leu Thr Ile
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157 Cys Ala Lys Ser Leu Ala Val Lys Ala Glu Ala Met Lys Lys Arg Lys
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160 Phe Ser
161          210
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167 <213> ORGANISM: Homo sapiens
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175 agtcccgcgc tgcaggatct gcaagccacg gaggccaatt gcacgggtgct gtcgggtgcag 180
176 cagatcggcg agtggttcga gtgcacctc acctgtggcg ccgactgcag gggcacctcg 240
177 cagtaccctt gcgtccaggt ctacgtgaac aactctgagt ccaactctag ggcgctgctg 300
178 cacagcgacg agcaccagct cctgaccaac cccaagtgtc cctatatccc tccctgtaag 360
179 agagaaaatc agaagaattt ggaaagtgtc atgaattggc aacagtactg gaaagatgag 420
180 attggttccc agccatttac ttgctatttt aatcaacatc aaagaccaga tgatgtgctt 480
181 ctgcatcgca ctcatgatga gattgtcctc ctgcattgct tcctctggcc cctgggtgaca 540
182 tttgtggtgg gcgttctcat tgtggtcctg accatctgtg ccaagagctt ggcgggtcaag 600
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187 <211> LENGTH: 235
188 <212> TYPE: PRT
189 <213> ORGANISM: Homo sapiens
191 <220> FEATURE:
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196 1          5          10          15
198 Glu Lys Arg Asn Ile Tyr Gln Lys Ile Arg Asp His Asp Leu Leu Asp
199          20          25          30
201 Lys Arg Lys Thr Val Thr Ala Leu Lys Ala Gly Glu Asp Arg Ala Ile

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202          35          40          45
204 Leu Leu Gly Leu Ala Met Met Val Cys Ser Ile Met Met Tyr Phe Leu
205          50          55          60
207 Leu Gly Ile Thr Leu Leu Arg Ser Tyr Met Gln Ser Val Trp Thr Glu
208 65          70          75          80
210 Glu Ser Gln Cys Thr Leu Leu Asn Ala Ser Ile Thr Glu Thr Phe Asn
211          85          90          95
213 Cys Ser Phe Ser Cys Gly Pro Asp Cys Trp Lys Leu Ser Gln Tyr Pro
214          100          105          110
216 Cys Leu Gln Val Tyr Val Asn Leu Thr Ser Ser Gly Glu Lys Leu Leu
217          115          120          125
219 Leu Tyr His Thr Glu Glu Thr Ile Lys Ile Asn Gln Lys Cys Ser Tyr
220          130          135          140
222 Ile Pro Lys Cys Gly Lys Asn Phe Glu Glu Ser Met Ser Leu Val Asn
223 145          150          155          160
225 Val Val Met Glu Asn Phe Arg Lys Tyr Gln His Phe Ser Cys Tyr Ser
226          165          170          175
228 Asp Pro Glu Gly Asn Gln Lys Ser Val Ile Leu Thr Lys Leu Tyr Ser
229          180          185          190
231 Ser Asn Val Leu Phe His Ser Leu Phe Trp Pro Thr Cys Met Met Ala
232          195          200          205
234 Gly Gly Val Ala Ile Val Ala Met Val Lys Leu Thr Gln Tyr Leu Ser
235          210          215          220
237 Leu Leu Cys Glu Arg Ile Gln Arg Ile Asn Arg
238 225          230          235
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244 <213> ORGANISM: Homo sapiens
246 <220> FEATURE:
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252 aaggcaggag aggaccgagc tattctcctg ggactggcta tgatgggtgtg ctccatcatg 180
253 atgtattttc tgctgggaat cacactcctg cgctcataca tgcagagcgt gtggaccgaa 240
254 gagtctcaat gcaccttgct gaatgcgtcc atcacggaaa catttaaytg ctcccttcagc 300
255 tgtggtccag actgctggaa actttctcag taccctgcc tccaggtgta cgtaaacctg 360
256 acttcttccg gggaaaagct cctcctctac cacacagaag agacaataaa aatcaatcag 420
257 aagtgtcctt atatacctaa atgtggaaaa aattttgaag aatccatgtc cctggtgaat 480
258 gttgtcatgg aaaacttcag gaagtatcaa cacttctcct gctattctga ccagaagga 540
259 aaccagaaga gtgttatcct aacmaaaactc tacagttcca acgtgctgtt ccattcactc 600
260 ttctggccaa cctgtatgat ggctgggggt gtggcaattg ttgccatggt gaaacttaca 660
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266 <212> TYPE: DNA
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269 <220> FEATURE:

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279 <212> TYPE: DNA
280 <213> ORGANISM: Artificial Sequence
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283 <223> OTHER INFORMATION: Description of Artificial Sequence:primer to
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286 <400> SEQUENCE: 8
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291 <211> LENGTH: 24
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293 <213> ORGANISM: Artificial Sequence
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305 <212> TYPE: DNA
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309 <223> OTHER INFORMATION: Description of Artificial Sequence:primer to
310     amplify BK beta 2
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317 <211> LENGTH: 27
318 <212> TYPE: DNA
319 <213> ORGANISM: Artificial Sequence
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322 <223> OTHER INFORMATION: Description of Artificial Sequence:primer to
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330 <211> LENGTH: 24
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332 <213> ORGANISM: Artificial Sequence
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338 <400> SEQUENCE: 12
339 atggcgaagc tccgggtggc ttac 24

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VERIFICATION SUMMARY

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